

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 15:28:38 ; Search time 40 Seconds

(Without alignments)
194.672 Million cell updates/sec

Title: US-09-924-102-2

Sequence: 1 MLSTHFLFTFLFTFLSYSL.....RMGGGGRGSGTADTGKFLS 81

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

1: PIR_73:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	11.1	475	T18487	hypothetical prote
2	8	9.9	285	I13858	alcohol sulfotrans
3	8	9.9	627	A40201	artifect-warnin s
4	7	8.6	19	S12268	Qa-2 antigen - mou
5	7	8.6	137	B96038	probable plasmid s
6	7	8.6	145	H75262	hypothetical prote
7	7	8.6	146	H97518	hypothetical prote
8	7	8.6	194	D84793	hypothetical prote
9	7	8.6	195	D84793	hypothetical prote
10	7	8.6	214	A27338	transcription regu
11	7	8.6	285	I146207	involucrin - dog
12	7	8.6	304	H64156	hypothetical prote
13	7	8.6	311	C71612	probable multiple-
14	7	8.6	337	S38166	hypothetical prote
15	7	8.6	368	A54430	hypothetical prote
16	7	8.6	380	T117236	hypothetical prote
17	7	8.6	381	H64795	citrate (pro-35)-
18	7	8.6	381	A90711	hypothetical prote
19	7	8.6	381	E85561	hypothetical prote
20	7	8.6	507	B84506	probable Athlia re
21	7	8.6	534	C84713	hypothetical prote
22	7	8.6	546	G86221	protein F7G19.14 l
23	7	8.6	606	A72429	oligopeptide ABC t
24	7	8.6	622	C84506	probable Athlia re
25	7	8.6	682	T28899	hypothetical prote
26	7	8.6	804	D69650	leucine-tRNA ligas
27	7	8.6	806	A84060	leucyl-tRNA synthe
28	7	8.6	808	T34357	hypothetical prote
29	7	8.6	850	T01847	hypothetical prote

30	7	8.6	1230	2	T07663	soluble starch syn
31	7	8.6	1430	2	T34516	hypothetical prote
32	6	7.4	65	2	A86027	hypothetical prote
33	6	7.4	69	2	S32028	Sp12 protein homol
34	6	7.4	70	2	A69842	hypothetical prote
35	6	7.4	72	2	T39894	very hypothetical
36	6	7.4	79	2	C87490	hypothetical prote
37	6	7.4	93	2	E70513	phosphoribosyl-ATP
38	6	7.4	96	2	T09310	thymidine Kinase h
39	6	7.4	101	2	C82133	hypothetical prote
40	6	7.4	118	2	T41419	40s ribosomal prot
41	6	7.4	128	2	F87353	conserved hypotnet
42	6	7.4	134	2	T13292	repressor protein
43	6	7.4	137	2	F97763	hypothetical prote
44	6	7.4	138	2	F75120	hypothetical prote
45	6	7.4	140	2	JC1253	ribosomal protein

ALIGNMENTS

RESULT 1

T18487

hypothetical protein C0830W - malaria parasite (Plasmodium falciparum)

C:Species: Plasmodium falciparum

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2002

C:Accession: T18487

R:Lawson, D.; Bowman, S.; Barrell, B.

submitted to the EMBL Data Library, August 1997

A:Reference number: Z18935

A:Accession: T18487

A:Status: preliminary; translated from GB/EMBL/DBDf

A:Molecule type: DNA

A:Residues: 1-475 <LAW>

A:Cross-references: EMBL:Z98551; NID:e1331903; PIDN:CAB1126.1

C:Genetics:

A:Map position: 3

A:Introns: 112/2

A:Note: C0830W

Query Match 11.1%; Score 9; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LFYLFYTF 15
Db 115 LFYLFYTF 123

RESULT 2

I38548

alcohol sulfotransferase (EC 2.8.2.2) - human

N:Alternate names: dehydroepiandrosterone sulfotransferase (DHEA-ST); dehydroepiandro

C:Species: Homo sapiens (man)

C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 11-Jun-1999

C:Accession: I53037; I38548; I38549; JCI223; S28155; A58735; I37285; S52476

R:Lin-Tse, V.; Dufort, I.; Paquet, N.; Reimnitz, G.; Labrie, F.

DNA Cell Biol. 14, 511-518, 1995

A:Title: Structural characterization and expression of the human dehydroepiandroster

A:Reference number: I53037; MUID:95322029; PMID:7598806

A:Accession: I53037

A:Status: preliminary; translated from GB/EMBL/DBDf

A:Molecule type: DNA

A:Residues: 1-285 <LUD>

A:Cross-references: GB:I36196; NID:g908766; PIDN:AAA75491.1; PID:g908768

R:Osterness, D.M.; Wleiden, E.D.; Wood, T.C.; Watson, R.W.G.; Madden, B.J.; McCormick,

Mol. Pharmacol. 41, 865-872, 1992

A:Title: Human liver dehydroepiandrosterone sulfotransferase: Molecular cloning and e

A:Reference number: I38548; MUID:92269778; PMID:1588921

A:Accession: I38548

A:Status: translated from GB/EMBL/DBDf

A:Molecule type: mRNA

A:Residues: 1-285 <OTT1>

A:Cross-references: EMBL:U08024; NID:9468250; PIDN:AAA17749.1; PID:9468251
 A:Accession: I38549
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-285 <ORF2>
 A:Cross-references: EMBL:U08025; NID:9468252; PIDN:AAA17750.1; PID:9468253
 A:Note: parts of this sequence were determined by protein sequencing; the amino end of t
 A:Note: three electrophoretic forms were observed
 R:Kong, A.N.T.; Yang, L.; Ma, M.; Tao, D.; Bjornsson, T.D.
 Biochem. Biophys. Res. Commun. 187, 448-454, 1992
 A:Title: Molecular cloning of the alcohol/hydroxysteroid form (hSta) of sulfotransferase
 A:Reference number: JCI1223; PMID:92352364; PMID:1520333
 A:Accession: JCI1223
 A:Molecule type: mRNA
 A:Residues: 1-158, 'V', 160-285 <CON>
 A:Cross-references: GB:S43859; NID:9255072
 A:Experimental source: liver
 A:Note: the authors translated the codon AGC for residue 222 as Thr
 R:Comer, K.A.; Falany, J.L.; Falany, C.N.
 Biochem. J. 289, 233-240, 1993
 A:Title: Cloning and expression of human liver dehydroepiandrosterone sulphotransferase.
 A:Reference number: S28155; PMID:93143674; PMID:7678732
 A:Accession: S28155
 A:Molecule type: mRNA
 A:Residues: 1-89, 'S', 91-285 <CON>
 A:Cross-references: GB:S53620; NID:9312804; PIDN:CAA49755.1; PID:9312805; GB:
 A:Note: parts of this sequence were determined by protein sequencing; the amino end of t
 R:Forbes, K.J.; Hagen, M.; Glaty, H.; Hume, R.; Coughtrie, M.W.
 Mol. Cell. Endocrinol. 112, 53-60, 1995
 A:Title: Human fetal adrenal hydroxysteroid sulphotransferase: cDNA cloning, stable expr
 A:Reference number: A58735; PMID:96034512; PMID:7589785
 A:Accession: A58735
 A:Molecule type: mRNA
 A:Residues: 1-285 <ORF>
 A:Cross-references: GB:X84816; NID:9683577; PIDN:CAA59274.1; PID:9683578
 A:Experimental source: fetal adrenal
 R:O'Brien, D.M.; Her, C.; Assoy, S.; Kimura, S.; Wieben, E.D.; Weinshtilboun, R.M.
 DNA Cell Biol. 14, 331-341, 1995
 A:Title: Human dehydroepiandrosterone sulphotransferase gene: molecular cloning and struc
 A:Reference number: 137285; PMID:95225980; PMID:7710689
 A:Accession: 137285
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-285 <RES>
 A:Cross-references: EMBL:U13061; NID:9806716; PIDN:AA051353.1; PID:9806718
 C:Genetics:
 A:Gene: GDB:SND; HST
 A:Cross-references: GDB:132655; OMIM:125263
 A:Map position: 19q13.3-19q13.3
 A:Introns: 46/1; 115/3; 158/1; 189/3; 249/1
 C:Complex: homodimer
 C:Function:
 A:Description: catalyzes formation of the sulfate esters of alcohols using 3'-phosphoad
 A:Pathway: steroid metabolism: detoxification
 A:Note: sulfates bile acids and steroids, in particular dehydroepiandrosterone, in the l
 C:Superfamily: alcohol sulphotransferase
 C:Keywords: acetylated amino end; detoxification; homodimer; steroid metabolism; sulfot
 F:2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted

Query Match 9.9%; Score 8; DB 1; Length 285;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 48 FRSETLRK 55
 DB 18 FRSETLRK 25

RESULT 3
 A40201
 artifact-warning sequence (translated ALU class A) - human
 C:Species: Homo sapiens (man)
 C:Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000

C:Accession: A40201
 R:Clavert, J.M.
 Personal communication, 1992
 A:Reference number: A40201
 A:Accession: A40201
 A:Molecule type: DNA
 A:Residues: 1-627 <CIA>
 R:Clavert, J.M.
 Genomics 12, 838-841, 1992
 A:Title: Identifying coding exons by similarity search: Alu-derived and other potenti
 A:Reference number: A40200; PMID:92241891; PMID:1572661
 A:Contents: annotation
 C:Comment: This "warning" entry is a conceptual translation in all 6 reading frames o
 in-frame stop codons are shown as 'x'.
 C:Comment: Any significant similarity of a predicted protein sequence to a portion of

Query Match 9.9%; Score 8; DB 4; Length 627;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 SLGDRARL 26
 DB 293 SLGDRARL 300

RESULT 4
 Qa-2 antigen - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
 C:Accession: S12268
 R:Ulker, N.; Lewis, K.D.; Hood, L.E.; Stroyanowski, I.
 EMBO J. 9, 3839-3847, 1990
 A:Title: Activated T cells transcribe an alternatively spliced mRNA encoding a solubl
 A:Reference number: S12268; PMID:91065311; PMID:2249652
 A:Accession: S12268
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-19 <UNK>
 A:Cross-references: GB:X57330; NID:9288506; PIDN:CAA0607.1; PID:9288508

Query Match 8.6%; Score 7; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 RMGGGG 68
 DB 6 RMGGGG 12

RESULT 5
 B96038
 probable plasmid stability protein [imported] - Sinorhizobium meliloti (strain 1021)
 C:Species: Sinorhizobium meliloti
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: B96038
 R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Her
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A:Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing e
 A:Reference number: A95842; PMID:21396508; PMID:11481431
 A:Accession: B96038
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-137 <UNK>
 A:Cross-references: GB:AL591985; PIDN:CAC49970.1; PID:915141458; GSPDB:GN00167
 A:Experimental source: strain 1021, megaplasmid pSymB
 R:Calbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hub
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
 hebaunt, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Welis, D.H.; Wong, K.; Yeh,

A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SMD21651
A:Genome: plasmid

Query Match 8.6%; Score 7; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 50 SEFLRKT 56
Db 10 SEFLRKT 16

RESULT 6
H75262
hypothetical protein - *Deinococcus radiodurans* (strain R1)
C:Species: *Deinococcus radiodurans*
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: H75262
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S.; Shen, M.; Vamathevan, J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: H75262
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-145 <WHI>
A:Cross-references: GB:AE002082; GB:AE00513; NID:g4640347; PIDN:AMF12073.1; PID:g464035
C:Genetics:
A:Experimental source: strain R1
A:Gene: DR2529
A:Map position: 1

Query Match 8.6%; Score 7; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 67 GGRGRTA 73
Db 128 GGRGRTA 134

RESULT 7
H97518
hypothetical protein AGR_C_2417 [imported] - *Agrobacterium tumefaciens* (strain C58, Cere
C:Species: *Agrobacterium tumefaciens*
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C:Accession: H97518
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*
A:Reference number: A97359; PMID:11743194
A:Accession: H97518
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-146 <KUR>
A:Cross-references: GB:AE007869; PIDN:AMK87105.1; PID:g15156367; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C_2417
A:Map position: circular chromosome

Query Match 8.6%; Score 7; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 74 DTGGMFL 80
Db 1111111

Db 20 DTGGMFL 26

RESULT 8
D84793
hypothetical protein At2g37490 [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cross)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: D84793
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shee, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: D84793
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-194 <STO>
A:Cross-references: GB:AE002093; NID:g4056499; PIDN:AMC98065.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g37490
A:Map position: 2

Query Match 8.6%; Score 7; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 54 RKTGKKG 60
Db 146 RKTGKKG 152

RESULT 9
T28773
hypothetical protein E03H12.4 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T28773
R:Nelson, J.; Wohldmann, P.; Sansone, J.
submitted to the EMBL Data Library, June 1997
A:Description: The sequence of C. elegans cosmid E03H12.
A:Reference number: Z20520
A:Accession: T28773
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-195 <NEU>
A:Cross-references: EMBL:AF000299; PIDN:AAQ47979.1; GSPDB:GN00022; CESP:E03H12.4
A:Experimental source: strain Bristol N2; clone E03H12
C:Genetics:
A:Gene: CESP:E03H12.4
A:Map position: 4
A:Introns: 17/3; 70/3; 111/3; 150/1

Query Match 8.6%; Score 7; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 7 LFYLFY 13
Db 4 LFYLFY 10

RESULT 10
AB2738
transcription regulator, Tetr family Atu1314 [imported] - *Agrobacterium tumefaciens* (
C:Species: *Agrobacterium tumefaciens*
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C:Accession: AB2738
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayvin, T.; Levy, R.; Li, M.; McCl
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, B.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; PMID:11743193
 A:Accession: AB2738
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-214 <KUR>
 A:Cross-references: GB:AE008688; PIDN:AAL42320.1; PID:g17739723; GSPDB:GN00186
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atul314
 A:Map position: circular chromosome

Query Match 8.6%; Score 7; DB 2; Length 214;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 74 DTGMFL 80
 DB 88 DTGMFL 94

RESULT 11
 I46207
 Involutrin - dog
 C:Species: Canis lupus familiaris (dog)
 C>Date: 16-Aug-1996 #sequence_revision 23-Aug-1996 #text_change 22-Jun-1999
 C:Accession: I46207
 R:Tseng, H.; Green, H.
 Mol. Biol. Evol. 7, 293-302, 1990
 A:Title: The Involutrin genes of pig and dog: comparison of their segments of repeats w
 A:Reference number: I46207; MUID:90348475; PMID:2385171
 A:Accession: I46207
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1285 <TSE>
 A:Cross-references: GB:M34442; NID:g163980; PIDN:AAA30853.1; PID:g163981
 C:Comment: During the terminal differentiation of keratinocytes, this protein from the c
 lined envelope under the plasma membrane.
 C:Superfamily: Involutrin
 C:Keywords: cornified cell envelope; duplication; epidermis; tandem repeat

Query Match 8.6%; Score 7; DB 1; Length 285;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 32 KOQKQEO 38
 DB 198 KOQKQEO 204

RESULT 12
 H64156
 hypothetical protein H10687 - Haemophilus influenzae (strain Rd KW20)
 C:Species: Haemophilus influenzae
 C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 21-Jul-2000
 C:Accession: H64156
 R:Flaeschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
 ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
 .D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
 Science 269, 496-512, 1995
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
 A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
 A:Reference number: A64000; MUID:95350630; PMID:7542800
 A:Accession: H64156
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-304 <TIGR>
 A:Cross-references: GB:U32751; GB:I42023; NID:g3212200; PIDN:AAC22347.1; PID:g1573689; T
 A:Note: best homolog was a hypothetical protein from Bacillus subtilis

Query Match 8.6%; Score 7; DB 2; Length 304;

Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 LFYLFPI 13
 DB 71 LFYLFPI 77

RESULT 13
 C71612
 Probable multiple-TM membrane protein PFB0535w - malaria parasite (Plasmodium falci
 C:Species: Plasmodium falciparum
 C>Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
 C:Accession: C71612
 R:Gardner, M.J.; Tettelin, H.; Carnocci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.
 .; Perera, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H
 Science 282, 1126-1132, 1998
 A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
 A:Reference number: A71600; MUID:99021743; PMID:9804551
 A:Accession: C71612
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-311 <GAR>
 A:Cross-references: GB:AE001401; GB:AE001362; NID:g3845209; PIDN:AAC71896.1; PID:g384
 A:Experimental source: clone 3D7
 C:Genetics:
 A:Gene: PFB0535w

Query Match 8.6%; Score 7; DB 2; Length 311;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 LFYLFPI 13
 DB 205 LFYLFPI 211

RESULT 14
 S38166
 hypothetical protein YKR088c - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein YKR408
 C:Species: Saccharomyces cerevisiae
 C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 19-Apr-2002
 C:Accession: S38166; S42017; S39129
 R:Baladron, V.; Ballester, J.P.G.; Bou, G.; del Rey, F.; Esteban, P.F.; Garcia-Cantale
 submitted to the Protein Sequence Database, March 1994
 A:Reference number: S38158
 A:Accession: S38166
 A:Molecule type: DNA
 A:Residues: 1-337 <BAL>
 A:Cross-references: EMBL:Z28313; NID:g486572; PIDN:CAA82167.1; PID:g486573; MIPS:YKR0
 A:Experimental source: strain S288C
 R:Garcia-Cantalejo, J.; Baladron, V.; Esteban, P.F.; Santos, M.A.; Bou, G.; Remacha,
 yeast 10, 231-245, 1994
 A:Title: The complete sequence of an 18,002 bp segment of Saccharomyces cerevisiae ch
 A:Reference number: S42009; MUID:94262327; PMID:8203164
 A:Accession: S42017
 A:Molecule type: DNA
 A:Residues: 1-337 <GAR>
 A:Cross-references: EMBL:Z27116; NID:g415899; PIDN:CAA81639.1; PID:g415908
 A:Experimental source: strain S288C
 C:Genetics:
 A:Cross-references: SGD:S0001796
 A:Map position: 11R
 C:Keywords: transmembrane protein
 F:96-112/Domain: transmembrane #status predicted <TM1>
 F:138-134/Domain: transmembrane #status predicted <TM2>
 F:174-190/Domain: transmembrane #status predicted <TM3>
 F:290-306/Domain: transmembrane #status predicted <TM4>

Query Match 8.6%; Score 7; DB 2; Length 337;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 LEIYLF1 13
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 Db 264 LEIYLF1 270

RESULT 15

A54430
 hypoxic function transcription repressor ROX1 - yeast (Saccharomyces cerevisiae)
 N:Alternate names: DNA-binding protein ROX1; protein YP9499.20; protein YPR065W
 C:Species: Saccharomyces cerevisiae
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
 C/Accession: A54430; S54086; S55246; S17015
 R:Balasubramanian, B.; Lowry, C.V.; Zitomer, R.S.
 Mol. Cell. Biol. 13, 6071-6078, 1993
 A>Title: The Rox1 repressor of the Saccharomyces cerevisiae hypoxic genes is a specific
 A:Reference number: A54430; MUID:94019282; PMID:8413209
 A:Accession: A54430
 A:Molecule type: DNA
 A:Residues: 1-368 <BAL>
 R:Badcock, K.; Churcher, C.M.
 A:Cross-references: EMBL:X60458; NID:q4361; PIDN:CAA42991.1; PID:q4362
 submitted to the EMBL Data Library, May 1995
 A:Reference number: S54067
 A:Accession: S54067
 A:Molecule type: DNA
 A:Residues: 1-368 <BAD>
 A:Cross-references: EMBL:Z49219; NID:q805025; PIDN:CAA89182.1; PID:q805045; MIPS:YPR065W
 R:Decker, J.; Perini, R.; Balasubramanian, B.; Zitomer, R.S.
 Genetics 139, 1149-1158, 1995
 A>Title: Multiple elements and auto-repression regulate Rox1, a repressor of hypoxic gen
 A:Reference number: S55246; MUID:95286046; PMID:7768429
 A:Accession: S55246
 A:Molecule type: DNA
 A:Residues: 1-17 <DEC>
 C:Genetics:
 A:Gene: SGD:ROX1
 A:Cross-references: SGD:S0006269; MIPS:YPR065W
 A:Map position: 16R
 C:Superfamily: unassigned HMG box proteins; HMG box homology
 C:Keywords: DNA binding; transcription regulation
 F:8-87/Domain: HMG box homology <HMG1>

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 Db 106 QOQKEQQ 112

Search completed: May 29, 2003, 15:33:24
 Job time : 43 secs

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